

SEQUENCE LISTING

<110> Napier, Johnathan A.
Sayanova, Olga
Lazarus, Colin M.
Qi, Baoxiu
Heinz, Ernst
Zank, Thorsten
Zahringer, Ulrich

<120> Novel method for the production of polyunsaturated fatty acids

<130> 13478-00001-US

<150> PCT/EP2003/014054

<151> 2003-12-11

<150> GB 0229578.0

<151> 2002-12-19

<150> GB 0316989.3

<151> 2003-07-21

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 1266

<212> DNA

<213> Euglena gracilis

<220>

<221> CDS

<222> (1)..(1266)

<223> delta-8-desaturase

<400> 1

atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca	48
Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr	
1 5 10 15	

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att	96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile	
20 25 30	

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg	144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met	
35 40 45	

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat	192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn	
50 55 60	

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag	240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu	
65 70 75 80	

gat	ttc	cgg	aag	ctc	cga	gaa	gag	ttg	atc	gca	act	ggc	atg	ttt	gat	288
Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp	
			85					90						95		
gcc	tcc	ccc	ctc	tgg	tac	tca	tac	aaa	atc	agc	acc	aca	ctg	ggc	ctt	336
Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu	
			100					105					110			
gga	gtg	ctg	ggg	tat	ttc	ctg	atg	gtt	cag	tat	cag	atg	tat	ttc	att	384
Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile	
		115					120					125				
ggg	gca	gtg	ttg	ctt	ggg	atg	cac	tat	caa	cag	atg	ggc	tgg	ctt	tct	432
Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser	
	130					135					140					
cat	gac	att	tgc	cac	cac	cag	act	ttc	aag	aac	cgg	aac	tgg	aac	aac	480
His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn	
145					150					155					160	
ctc	gtg	gga	ctg	gta	ttt	ggc	aat	ggg	ctg	caa	ggg	ttt	tcc	gtg	aca	528
Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr	
				165				170						175		
tgc	tgg	aag	gac	aga	cac	aat	gca	cat	cat	tcg	gca	acc	aat	gtt	caa	576
Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln	
			180					185					190			
ggg	cac	gac	cct	gat	att	gac	aac	ctc	ccc	ctc	tta	gcc	tgg	tct	gag	624
Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu	
		195					200					205				
gat	gac	gtc	aca	cgg	gcg	tca	ccg	att	tcc	cgc	aag	ctc	att	cag	ttc	672
Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe	
	210					215					220					
cag	cag	tat	tat	ttc	ttg	gtc	atc	tgt	atc	ttg	ttg	cgg	ttc	att	tgg	720
Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp	
225					230					235					240	
tgt	ttc	cag	agc	gtg	ttg	acc	gtg	cgc	agt	ctg	aag	gac	aga	gat	aac	768
Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn	
				245				250						255		
caa	ttc	tat	cgc	tct	cag	tat	aag	aag	gag	gcc	att	ggc	ctc	gcc	ctg	816
Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu	
			260					265					270			
cat	tgg	aca	ttg	aag	gcc	ctg	ttc	cac	tta	ttc	ttt	atg	ccc	agc	atc	864
His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile	
		275					280					285				
ctc	aca	tcg	ctg	ttg	gta	ttt	ttc	gtt	tcg	gag	ctg	gtt	ggc	ggc	ttc	912
Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe	
	290					295					300					

ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc 960
 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
 305 310 315 320
 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat 1008
 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
 325 330 335
 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga 1056
 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
 340 345 350
 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc 1104
 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
 355 360 365
 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag 1152
 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
 370 375 380
 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc 1200
 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
 385 390 395 400
 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc 1248
 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
 405 410 415
 gcg ggg aag gct cta taa 1266
 Ala Gly Lys Ala Leu
 420

<210> 2
 <211> 421
 <212> PRT
 <213> *Euglena gracilis*

<400> 2
 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15
 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20 25 30
 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45
 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60
 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80
 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85 90 95

Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu		
			100					105					110				
Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile		
		115					120					125					
Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser		
	130					135					140						
His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn		
145					150					155					160		
Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr		
				165					170						175		
Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln		
			180					185					190				
Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu		
	195						200					205					
Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe		
	210					215					220						
Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp		
225					230					235					240		
Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn		
				245					250					255			
Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu		
			260					265					270				
His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile		
	275						280					285					
Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe		
	290					295					300						
Gly	Ile	Ala	Ile	Val	Val	Phe	Met	Asn	His	Tyr	Pro	Leu	Glu	Lys	Ile		
305					310					315					320		
Gly	Asp	Ser	Val	Trp	Asp	Gly	His	Gly	Phe	Ser	Val	Gly	Gln	Ile	His		
			325						330					335			
Glu	Thr	Met	Asn	Ile	Arg	Arg	Gly	Ile	Ile	Thr	Asp	Trp	Phe	Phe	Gly		
			340					345					350				
Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Trp	Pro	Thr	Leu	Pro	Arg		
		355					360					365					
His	Asn	Leu	Thr	Ala	Val	Ser	Tyr	Gln	Val	Glu	Gln	Leu	Cys	Gln	Lys		
	370					375					380						
His	Asn	Leu	Pro	Tyr	Arg	Asn	Pro	Leu	Pro	His	Glu	Gly	Leu	Val	Ile		
385					390					395					400		

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
 405 410 415

Ala Gly Lys Ala Leu
 420

<210> 3

<211> 777

<212> DNA

<213> *Isochrysis galbana*

<220>

<221> CDS

<222> (1) .. (777)

<223> delta-9-elongase

<400> 3

atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc 48
 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
 1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
 20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
 35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
 50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
 65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
 85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
 100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
 115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
 130 135 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
 145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
165 170 175

acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
180 185 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
195 200 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct 672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
210 215 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt 720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225 230 235 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag 768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
245 250 255

cag ctc tag 777
Gln Leu

<210> 4

<211> 258

<212> PRT

<213> Isochrysis galbana

<400> 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1 5 10 15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65 70 75 80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu

115					120					125						
Arg	Val	Ser	Phe	Leu	Gln	Ala	Phe	His	His	Phe	Gly	Ala	Pro	Trp	Asp	
130					135					140						
Val	Tyr	Leu	Gly	Ile	Arg	Leu	His	Asn	Glu	Gly	Val	Trp	Ile	Phe	Met	
145					150					155					160	
Phe	Phe	Asn	Ser	Phe	Ile	His	Thr	Ile	Met	Tyr	Thr	Tyr	Tyr	Gly	Leu	
165					170					175						
Thr	Ala	Ala	Gly	Tyr	Lys	Phe	Lys	Ala	Lys	Pro	Leu	Ile	Thr	Ala	Met	
180					185					190						
Gln	Ile	Cys	Gln	Phe	Val	Gly	Gly	Phe	Leu	Leu	Val	Trp	Asp	Tyr	Ile	
195					200					205						
Asn	Val	Pro	Cys	Phe	Asn	Ser	Asp	Lys	Gly	Lys	Leu	Phe	Ser	Trp	Ala	
210					215					220						
Phe	Asn	Tyr	Ala	Tyr	Val	Gly	Ser	Val	Phe	Leu	Leu	Phe	Cys	His	Phe	
225					230					235					240	
Phe	Tyr	Gln	Asp	Asn	Leu	Ala	Thr	Lys	Lys	Ser	Ala	Lys	Ala	Gly	Lys	
245					250					255						

Gln Leu

<210> 5
 <211> 1410
 <212> DNA
 <213> Phaeodactylum tricornutum

<220>
 <221> CDS
 <222> (1)..(1410)
 <223> delta-5-desaturase

<400> 5																
atg	gct	ccg	gat	gcg	gat	aag	ctt	cga	caa	cgc	cag	acg	act	gcg	gta	48
Met	Ala	Pro	Asp	Ala	Asp	Lys	Leu	Arg	Gln	Arg	Gln	Thr	Thr	Ala	Val	
1				5				10						15		
gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt																96
Ala	Lys	His	Asn	Ala	Ala	Thr	Ile	Ser	Thr	Gln	Glu	Arg	Leu	Cys	Ser	
			20					25					30			
ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat																144
Leu	Ser	Ser	Leu	Lys	Gly	Glu	Glu	Val	Cys	Ile	Asp	Gly	Ile	Ile	Tyr	
			35				40					45				
gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt																192
Asp	Leu	Gln	Ser	Phe	Asp	His	Pro	Gly	Gly	Glu	Thr	Ile	Lys	Met	Phe	
			50				55					60				
ggg ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat																240

Gly 65	Gly	Asn	Asp	Val	Thr 70	Val	Gln	Tyr	Lys	Met 75	Ile	His	Pro	Tyr	His 80	
acc	gag	aag	cat	ttg	gaa	aag	atg	aag	cgt	gtc	ggc	aag	gtg	acg	gat	288
Thr	Glu	Lys	His	Leu	Glu	Lys	Met	Lys	Arg	Val	Gly	Lys	Val	Thr	Asp	
				85					90					95		
ttc	gtc	tgc	gag	tac	aag	ttc	gat	acc	gaa	ttt	gaa	cgc	gaa	atc	aaa	336
Phe	Val	Cys	Glu	Tyr	Lys	Phe	Asp	Thr	Glu	Phe	Glu	Arg	Glu	Ile	Lys	
			100					105					110			
cga	gaa	gtc	ttc	aag	att	gtg	cga	cga	ggc	aag	gat	ttc	ggg	act	ttg	384
Arg	Glu	Val	Phe	Lys	Ile	Val	Arg	Arg	Gly	Lys	Asp	Phe	Gly	Thr	Leu	
		115					120					125				
gga	tgg	ttc	ttc	cgt	gcg	ttt	tgc	tac	att	gcc	att	ttc	ttc	tac	ctg	432
Gly	Trp	Phe	Phe	Arg	Ala	Phe	Cys	Tyr	Ile	Ala	Ile	Phe	Phe	Tyr	Leu	
	130					135					140					
cag	tac	cat	tgg	gtc	acc	acg	gga	acc	tct	tgg	ctg	ctg	gcc	gtg	gcc	480
Gln	Tyr	His	Trp	Val	Thr	Thr	Gly	Thr	Ser	Trp	Leu	Leu	Ala	Val	Ala	
145					150					155					160	
tac	gga	atc	tcc	caa	gcg	atg	att	ggc	atg	aat	gtc	cag	cac	gat	gcc	528
Tyr	Gly	Ile	Ser	Gln	Ala	Met	Ile	Gly	Met	Asn	Val	Gln	His	Asp	Ala	
				165					170					175		
aac	cac	ggg	gcc	acc	tcc	aag	cgt	ccc	tgg	gtc	aac	gac	atg	cta	ggc	576
Asn	His	Gly	Ala	Thr	Ser	Lys	Arg	Pro	Trp	Val	Asn	Asp	Met	Leu	Gly	
			180					185					190			
ctc	ggg	gcg	gat	ttt	att	ggg	ggg	tcc	aag	tgg	ctc	tgg	cag	gaa	caa	624
Leu	Gly	Ala	Asp	Phe	Ile	Gly	Gly	Ser	Lys	Trp	Leu	Trp	Gln	Glu	Gln	
		195					200					205				
cac	tgg	acc	cac	cac	gct	tac	acc	aat	cac	gcc	gag	atg	gat	ccc	gat	672
His	Trp	Thr	His	His	Ala	Tyr	Thr	Asn	His	Ala	Glu	Met	Asp	Pro	Asp	
	210					215					220					
agc	ttt	ggg	gcc	gaa	cca	atg	ctc	cta	ttc	aac	gac	tat	ccc	ttg	gat	720
Ser	Phe	Gly	Ala	Glu	Pro	Met	Leu	Leu	Phe	Asn	Asp	Tyr	Pro	Leu	Asp	
225					230					235					240	
cat	ccc	gct	cgt	acc	tgg	cta	cat	cgc	ttt	caa	gca	ttc	ttt	tac	atg	768
His	Pro	Ala	Arg	Thr	Trp	Leu	His	Arg	Phe	Gln	Ala	Phe	Phe	Tyr	Met	
				245				250						255		
ccc	gtc	ttg	gct	gga	tac	tgg	ttg	tcc	gct	gtc	ttc	aat	cca	caa	att	816
Pro	Val	Leu	Ala	Gly	Tyr	Trp	Leu	Ser	Ala	Val	Phe	Asn	Pro	Gln	Ile	
			260					265					270			
ctt	gac	ctc	cag	caa	cgc	ggc	gca	ctt	tcc	gtc	ggg	atc	cgt	ctc	gac	864
Leu	Asp	Leu	Gln	Gln	Arg	Gly	Ala	Leu	Ser	Val	Gly	Ile	Arg	Leu	Asp	
		275					280					285				
aac	gct	ttc	att	cac	tcg	cga	cgc	aag	tat	gcg	gtt	ttc	tgg	cgg	gct	912
Asn	Ala	Phe	Ile	His	Ser	Arg	Arg	Lys	Tyr	Ala	Val	Phe	Trp	Arg	Ala	

290	295	300	
gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc			960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly			
305	310	315	320
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg			1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val			
	325	330	335
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc			1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe			
	340	345	350
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa			1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu			
	355	360	365
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt			1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly			
	370	375	380
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa			1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu			
385	390	395	400
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc			1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala			
	405	410	415
ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac			1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr			
	420	425	430
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac			1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His			
	435	440	445
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc			1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro			
	450	455	460
ttg acc gga cgg gcg taa			1410
Leu Thr Gly Arg Ala			
465			

<210> 6

<211> 469

<212> PRT

<213> Phaeodactylum tricornutum

<400> 6

Met	Ala	Pro	Asp	Ala	Asp	Lys	Leu	Arg	Gln	Arg	Gln	Thr	Thr	Ala	Val
1				5					10					15	

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser

20					25					30					
Leu	Ser	Ser	Leu	Lys	Gly	Glu	Glu	Val	Cys	Ile	Asp	Gly	Ile	Ile	Tyr
		35					40					45			
Asp	Leu	Gln	Ser	Phe	Asp	His	Pro	Gly	Gly	Glu	Thr	Ile	Lys	Met	Phe
	50					55					60				
Gly	Gly	Asn	Asp	Val	Thr	Val	Gln	Tyr	Lys	Met	Ile	His	Pro	Tyr	His
	65					70					75				80
Thr	Glu	Lys	His	Leu	Glu	Lys	Met	Lys	Arg	Val	Gly	Lys	Val	Thr	Asp
				85					90					95	
Phe	Val	Cys	Glu	Tyr	Lys	Phe	Asp	Thr	Glu	Phe	Glu	Arg	Glu	Ile	Lys
			100					105					110		
Arg	Glu	Val	Phe	Lys	Ile	Val	Arg	Arg	Gly	Lys	Asp	Phe	Gly	Thr	Leu
		115					120					125			
Gly	Trp	Phe	Phe	Arg	Ala	Phe	Cys	Tyr	Ile	Ala	Ile	Phe	Phe	Tyr	Leu
	130					135					140				
Gln	Tyr	His	Trp	Val	Thr	Thr	Gly	Thr	Ser	Trp	Leu	Leu	Ala	Val	Ala
	145					150					155				160
Tyr	Gly	Ile	Ser	Gln	Ala	Met	Ile	Gly	Met	Asn	Val	Gln	His	Asp	Ala
				165					170					175	
Asn	His	Gly	Ala	Thr	Ser	Lys	Arg	Pro	Trp	Val	Asn	Asp	Met	Leu	Gly
			180					185					190		
Leu	Gly	Ala	Asp	Phe	Ile	Gly	Gly	Ser	Lys	Trp	Leu	Trp	Gln	Glu	Gln
		195					200					205			
His	Trp	Thr	His	His	Ala	Tyr	Thr	Asn	His	Ala	Glu	Met	Asp	Pro	Asp
	210					215					220				
Ser	Phe	Gly	Ala	Glu	Pro	Met	Leu	Leu	Phe	Asn	Asp	Tyr	Pro	Leu	Asp
	225					230					235				240
His	Pro	Ala	Arg	Thr	Trp	Leu	His	Arg	Phe	Gln	Ala	Phe	Phe	Tyr	Met
				245					250					255	
Pro	Val	Leu	Ala	Gly	Tyr	Trp	Leu	Ser	Ala	Val	Phe	Asn	Pro	Gln	Ile
			260					265					270		
Leu	Asp	Leu	Gln	Gln	Arg	Gly	Ala	Leu	Ser	Val	Gly	Ile	Arg	Leu	Asp
		275					280					285			
Asn	Ala	Phe	Ile	His	Ser	Arg	Arg	Lys	Tyr	Ala	Val	Phe	Trp	Arg	Ala
	290					295					300				
Val	Tyr	Ile	Ala	Val	Asn	Val	Ile	Ala	Pro	Phe	Tyr	Thr	Asn	Ser	Gly
	305					310					315				320
Leu	Glu	Trp	Ser	Trp	Arg	Val	Phe	Gly	Asn	Ile	Met	Leu	Met	Gly	Val

325				330				335							
Ala	Glu	Ser	Leu	Ala	Leu	Ala	Val	Leu	Phe	Ser	Leu	Ser	His	Asn	Phe
340				345				350							
Glu	Ser	Ala	Asp	Arg	Asp	Pro	Thr	Ala	Pro	Leu	Lys	Lys	Thr	Gly	Glu
355				360				365							
Pro	Val	Asp	Trp	Phe	Lys	Thr	Gln	Val	Glu	Thr	Ser	Cys	Thr	Tyr	Gly
370				375				380							
Gly	Phe	Leu	Ser	Gly	Cys	Phe	Thr	Gly	Gly	Leu	Asn	Phe	Gln	Val	Glu
385				390				395				400			
His	His	Leu	Phe	Pro	Arg	Met	Ser	Ser	Ala	Trp	Tyr	Pro	Tyr	Ile	Ala
405				410				415							
Pro	Lys	Val	Arg	Glu	Ile	Cys	Ala	Lys	His	Gly	Val	His	Tyr	Ala	Tyr
420				425				430							
Tyr	Pro	Trp	Ile	His	Gln	Asn	Phe	Leu	Ser	Thr	Val	Arg	Tyr	Met	His
435				440				445							
Ala	Ala	Gly	Thr	Gly	Ala	Asn	Trp	Arg	Gln	Met	Ala	Arg	Glu	Asn	Pro
450				455				460							
Leu	Thr	Gly	Arg	Ala											
465															

```
<210> 7
<211> 1344
<212> DNA
<213> Ceratodon purpureus
```

```
<220>
<221> CDS
<222> (1)..(1344)
<223> delta-5-desaturase
```

<400> 7																	
atg	gta	tta	cga	gag	caa	gag	cat	gag	cca	ttc	ttc	att	aaa	att	gat	48	
Met	Val	Leu	Arg	Glu	Gln	Glu	His	Glu	Pro	Phe	Phe	Ile	Lys	Ile	Asp		
1				5					10					15			
gga	aaa	tgg	tgt	caa	att	gac	gat	gct	gtc	ctg	aga	tca	cat	cca	ggg	96	
Gly	Lys	Trp	Cys	Gln	Ile	Asp	Asp	Ala	Val	Leu	Arg	Ser	His	Pro	Gly		
			20					25					30				
ggt	agt	gca	att	act	acc	tat	aaa	aat	atg	gat	gcc	act	acc	gta	ttc	144	
Gly	Ser	Ala	Ile	Thr	Thr	Tyr	Lys	Asn	Met	Asp	Ala	Thr	Thr	Val	Phe		
		35					40				45						
cac	aca	ttc	cat	act	ggg	tct	aaa	gaa	gcg	tat	caa	tgg	ctg	aca	gaa	192	
His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu		
	50					55					60						

ttg	aaa	aaa	gag	tgc	cct	aca	caa	gaa	cca	gag	atc	cca	gat	att	aag	240
Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys	
65					70					75					80	
gat	gac	cca	atc	aaa	gga	att	gat	gat	gtg	aac	atg	gga	act	ttc	aat	288
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn	
				85					90					95		
att	tct	gag	aaa	cga	tct	gcc	caa	ata	aat	aaa	agt	ttc	act	gat	cta	336
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu	
			100					105					110			
cgt	atg	cga	gtt	cgt	gca	gaa	gga	ctt	atg	gat	gga	tct	cct	ttg	ttc	384
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe	
		115					120					125				
tac	att	aga	aaa	att	ctt	gaa	aca	atc	ttc	aca	att	ctt	ttt	gca	ttc	432
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe	
	130					135					140					
tac	ctt	caa	tac	cac	aca	tat	tat	ctt	cca	tca	gct	att	cta	atg	gga	480
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	
145					150					155					160	
gtt	gcg	tgg	caa	caa	ttg	gga	tgg	tta	atc	cat	gaa	ttc	gca	cat	cat	528
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His	
				165					170					175		
cag	ttg	ttc	aaa	aac	aga	tac	tac	aat	gat	ttg	gcc	agc	tat	ttc	gtt	576
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	
			180					185					190			
gga	aac	ttt	tta	caa	gga	ttc	tca	tct	ggt	ggt	tgg	aaa	gag	cag	cac	624
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	
		195					200					205				
aat	gtg	cat	cac	gca	gcc	aca	aat	gtt	gtt	gga	cga	gac	gga	gat	ctt	672
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	
	210					215					220					
gat	tta	gtc	cca	ttc	tat	gct	aca	gtg	gca	gaa	cat	ctc	aac	aat	tat	720
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	
225					230					235					240	
tct	cag	gat	tca	tgg	gtt	atg	act	cta	ttc	aga	tgg	caa	cat	gtt	cat	768
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	
				245					250					255		
tgg	aca	ttc	atg	tta	cca	ttc	ctc	cgt	ctc	tcg	tgg	ctt	ctt	cag	tca	816
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	
			260					265					270			
atc	att	ttt	gtt	agt	cag	atg	cca	act	cat	tat	tat	gac	tat	tac	aga	864
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	
		275					280					285				
aat	act	gcg	att	tat	gaa	cag	gtt	ggt	ctc	tct	ttg	cac	tgg	gct	tgg	912

Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	
290						295					300					
tca	ttg	ggg	caa	ttg	tat	ttc	cta	ccc	gat	tgg	tca	act	aga	ata	atg	960
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	
305					310					315					320	
ttc	ttc	ctt	gtt	tct	cat	ctt	gtt	gga	ggg	ttc	ctg	ctc	tct	cat	gta	1008
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	
				325					330					335		
gtt	act	ttc	aat	cat	tat	tca	gtg	gag	aag	ttt	gca	ttg	agc	tcg	aac	1056
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	
			340					345					350			
atc	atg	tca	aat	tac	gct	tgt	ctt	caa	atc	atg	acc	aca	aga	aat	atg	1104
Ile	Met	Ser	Asn	Tyr	Ala	Cys	Leu	Gln	Ile	Met	Thr	Thr	Arg	Asn	Met	
			355				360						365			
aga	cct	gga	aga	ttc	att	gac	tgg	ctt	tgg	gga	ggg	ctt	aac	tat	cag	1152
Arg	Pro	Gly	Arg	Phe	Ile	Asp	Trp	Leu	Trp	Gly	Gly	Leu	Asn	Tyr	Gln	
	370					375					380					
att	gag	cac	cat	ctt	ttc	cca	acg	atg	cca	cga	cac	aac	ttg	aac	act	1200
Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Thr	
385					390					395					400	
gtt	atg	cca	ctt	gtt	aag	gag	ttt	gca	gca	gca	aat	ggg	tta	cca	tac	1248
Val	Met	Pro	Leu	Val	Lys	Glu	Phe	Ala	Ala	Ala	Asn	Gly	Leu	Pro	Tyr	
				405					410					415		
atg	gtc	gac	gat	tat	ttc	aca	gga	ttc	tgg	ctt	gaa	att	gag	caa	ttc	1296
Met	Val	Asp	Asp	Tyr	Phe	Thr	Gly	Phe	Trp	Leu	Glu	Ile	Glu	Gln	Phe	
			420					425					430			
cga	aat	att	gca	aat	gtt	gct	gct	aaa	ttg	act	aaa	aag	att	gcc	tag	1344
Arg	Asn	Ile	Ala	Asn	Val	Ala	Ala	Lys	Leu	Thr	Lys	Lys	Ile	Ala		
		435					440					445				

<210> 8

<211> 447

<212> PRT

<213> Ceratodon purpureus

<400> 8

Met	Val	Leu	Arg	Glu	Gln	Glu	His	Glu	Pro	Phe	Phe	Ile	Lys	Ile	Asp	
1				5				10						15		
Gly	Lys	Trp	Cys	Gln	Ile	Asp	Asp	Ala	Val	Leu	Arg	Ser	His	Pro	Gly	
			20					25					30			
Gly	Ser	Ala	Ile	Thr	Thr	Tyr	Lys	Asn	Met	Asp	Ala	Thr	Thr	Val	Phe	
		35					40					45				
His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu	
	50					55					60					

Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys	65	70	75	80
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn	85	90	95	
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu	100	105	110	
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe	115	120	125	
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe	130	135	140	
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	145	150	155	160
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His	165	170	175	
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	180	185	190	
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	195	200	205	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	210	215	220	
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	225	230	235	240
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	245	250	255	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	260	265	270	
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	275	280	285	
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	290	295	300	
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	305	310	315	320
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	325	330	335	
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	340	345	350	
Ile	Met	Ser	Asn	Tyr	Ala	Cys	Leu	Gln	Ile	Met	Thr	Thr	Arg	Asn	Met	355	360	365	

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 9

<211> 1443

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (1) .. (1443)

<223> delta-5-desaturase

<220>

<221> misc_feature

<222> (317) .. (317)

<223> k is g or t/u

<220>

<221> misc_feature

<222> (361) .. (361)

<223> r is g or a

<400> 9

atg gcg ccc cac tct gcg gat act gct ggg ctc gtg cct tct gac gaa 48
 Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu
 1 5 10 15

ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96
 Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr
 20 25 30

ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144
 Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala
 35 40 45

gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192
 Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp
 50 55 60

att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag 240
 Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln
 65 70 75 80

gat	tcc	act	cag	ctt	ttc	gat	tcc	tat	cac	ccc	ctt	tat	gtc	agg	aaa	288
Asp	Ser	Thr	Gln	Leu	Phe	Asp	Ser	Tyr	His	Pro	Leu	Tyr	Val	Arg	Lys	
			85						90					95		
atg	ctc	gcg	aag	tac	tgt	att	ggg	gaa	tka	gta	ccg	tct	gct	ggt	gat	336
Met	Leu	Ala	Lys	Tyr	Cys	Ile	Gly	Glu	Xaa	Val	Pro	Ser	Ala	Gly	Asp	
			100					105					110			
gac	aag	ttt	aag	aaa	gca	act	ctg	rag	tat	gca	gat	gcc	gaa	aat	gaa	384
Asp	Lys	Phe	Lys	Lys	Ala	Thr	Leu	Xaa	Tyr	Ala	Asp	Ala	Glu	Asn	Glu	
		115					120					125				
gat	ttc	tat	ttg	gtt	gtg	aag	caa	cga	gtt	gaa	tct	tat	ttc	aag	agt	432
Asp	Phe	Tyr	Leu	Val	Val	Lys	Gln	Arg	Val	Glu	Ser	Tyr	Phe	Lys	Ser	
	130					135					140					
aac	aag	ata	aac	ccc	caa	att	cat	cca	cat	atg	atc	ctg	aag	tca	ttg	480
Asn	Lys	Ile	Asn	Pro	Gln	Ile	His	Pro	His	Met	Ile	Leu	Lys	Ser	Leu	
145					150					155					160	
ttc	att	ctt	ggg	gga	tat	ttc	gcc	agt	tac	tat	tta	gcg	ttc	ttc	tgg	528
Phe	Ile	Leu	Gly	Gly	Tyr	Phe	Ala	Ser	Tyr	Tyr	Leu	Ala	Phe	Phe	Trp	
			165						170					175		
tct	tca	agt	gtc	ctt	gtt	tct	ttg	ttt	ttc	gca	ttg	tgg	atg	ggg	ttc	576
Ser	Ser	Ser	Val	Leu	Val	Ser	Leu	Phe	Phe	Ala	Leu	Trp	Met	Gly	Phe	
			180					185					190			
ttc	gca	gcg	gaa	gtc	ggc	gtg	tcg	att	caa	cat	gat	gga	aat	cat	ggt	624
Phe	Ala	Ala	Glu	Val	Gly	Val	Ser	Ile	Gln	His	Asp	Gly	Asn	His	Gly	
		195					200					205				
tca	tac	act	aaa	tgg	cgt	ggc	ttt	gga	tat	atc	atg	gga	gcc	tcc	cta	672
Ser	Tyr	Thr	Lys	Trp	Arg	Gly	Phe	Gly	Tyr	Ile	Met	Gly	Ala	Ser	Leu	
	210					215					220					
gat	cta	gtc	gga	gcc	agt	agc	ttc	atg	tgg	aga	cag	caa	cac	gtt	gtg	720
Asp	Leu	Val	Gly	Ala	Ser	Ser	Phe	Met	Trp	Arg	Gln	Gln	His	Val	Val	
225					230					235					240	
gga	cat	cac	tcg	ttt	aca	aat	gtg	gac	aac	tac	gat	cct	gat	att	cgt	768
Gly	His	His	Ser	Phe	Thr	Asn	Val	Asp	Asn	Tyr	Asp	Pro	Asp	Ile	Arg	
				245					250					255		
gtg	aaa	gat	cca	gat	gtc	agg	agg	gtt	gcg	acc	aca	caa	cca	aga	caa	816
Val	Lys	Asp	Pro	Asp	Val	Arg	Arg	Val	Ala	Thr	Thr	Gln	Pro	Arg	Gln	
			260					265					270			
tgg	tat	cat	gcg	tat	cag	cat	atc	tac	ctg	gca	gta	tta	tat	gga	act	864
Trp	Tyr	His	Ala	Tyr	Gln	His	Ile	Tyr	Leu	Ala	Val	Leu	Tyr	Gly	Thr	
		275					280					285				
cta	gct	ctt	aag	agt	att	ttt	cta	gat	gat	ttc	ctt	gcg	tac	ttc	aca	912
Leu	Ala	Leu	Lys	Ser	Ile	Phe	Leu	Asp	Asp	Phe	Leu	Ala	Tyr	Phe	Thr	
	290					295					300					


```

gga tca att ggc cct gtc aag gtg gcg aaa atg acc ccc ctg gag ttc 960
Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe
305                      310                      315                      320

aac atc ttc ttt cag gga aag ctg cta tat gcg ttc tac atg ttc gtg 1008
Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val
                      325                      330                      335

ttg cca tct gtg tac ggt gtt cac tcc gga gga act ttc ttg gca cta 1056
Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu
                      340                      345                      350

tat gtg gct tct cag ctc att aca ggt tgg atg tta gct ttt ctt ttt 1104
Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe
                      355                      360                      365

caa gta gca cat gtc gtg gat gat gtt gca ttt cct aca cca gaa ggt 1152
Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly
                      370                      375                      380

ggg aag gtg aag gga gga tgg gct gca atg cag gtt gca aca act acg 1200
Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
385                      390                      395                      400

gat ttc agt cca cgc tca tgg ttc tgg ggt cat gtc tct gga gga tta 1248
Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
                      405                      410                      415

aac aac caa att gag cat cat ctg ttt cca gga gtg tgc cat gtt cat 1296
Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
                      420                      425                      430

tat cca gcc att cag cct att gtc gag aag acg tgc aag gaa ttc gat 1344
Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
                      435                      440                      445

gtg cct tat gta gcc tac cca act ttt tgg act gcg ttg aga gcc cac 1392
Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
                      450                      455                      460

ttt gcg cat ttg aaa aag gtt gga ttg aca gag ttt cgg ctc gat ggc 1440
Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
465                      470                      475                      480

tga 1443

```

<210> 10

<211> 480

<212> PRT

<213> *Physcomitrella patens*

<220>

<221> misc_feature

<222> (106)..(106)

<223> Xaa is unknown or other

<220>

<221> misc_feature

<222> (121)..(121)

<223> Xaa is unknown or other

<400> 10

Met	Ala	Pro	His	Ser	Ala	Asp	Thr	Ala	Gly	Leu	Val	Pro	Ser	Asp	Glu
1				5					10					15	

Leu	Arg	Leu	Arg	Thr	Ser	Asn	Ser	Lys	Gly	Pro	Glu	Gln	Glu	Gln	Thr
			20					25					30		

Leu	Lys	Lys	Tyr	Thr	Leu	Glu	Asp	Val	Ser	Arg	His	Asn	Thr	Pro	Ala
		35					40					45			

Asp	Cys	Trp	Leu	Val	Ile	Trp	Gly	Lys	Val	Tyr	Asp	Val	Thr	Ser	Trp
	50					55					60				

Ile	Pro	Asn	His	Pro	Gly	Gly	Ser	Leu	Ile	His	Val	Lys	Ala	Gly	Gln
65					70					75					80

Asp	Ser	Thr	Gln	Leu	Phe	Asp	Ser	Tyr	His	Pro	Leu	Tyr	Val	Arg	Lys
				85					90					95	

Met	Leu	Ala	Lys	Tyr	Cys	Ile	Gly	Glu	Xaa	Val	Pro	Ser	Ala	Gly	Asp
			100					105					110		

Asp	Lys	Phe	Lys	Lys	Ala	Thr	Leu	Xaa	Tyr	Ala	Asp	Ala	Glu	Asn	Glu
		115					120					125			

Asp	Phe	Tyr	Leu	Val	Val	Lys	Gln	Arg	Val	Glu	Ser	Tyr	Phe	Lys	Ser
	130					135						140			

Asn	Lys	Ile	Asn	Pro	Gln	Ile	His	Pro	His	Met	Ile	Leu	Lys	Ser	Leu
145					150					155					160

Phe	Ile	Leu	Gly	Gly	Tyr	Phe	Ala	Ser	Tyr	Tyr	Leu	Ala	Phe	Phe	Trp
			165						170					175	

Ser	Ser	Ser	Val	Leu	Val	Ser	Leu	Phe	Phe	Ala	Leu	Trp	Met	Gly	Phe
			180					185					190		

Phe	Ala	Ala	Glu	Val	Gly	Val	Ser	Ile	Gln	His	Asp	Gly	Asn	His	Gly
		195					200					205			

Ser	Tyr	Thr	Lys	Trp	Arg	Gly	Phe	Gly	Tyr	Ile	Met	Gly	Ala	Ser	Leu
	210					215					220				

Asp	Leu	Val	Gly	Ala	Ser	Ser	Phe	Met	Trp	Arg	Gln	Gln	His	Val	Val
225					230					235					240

Gly	His	His	Ser	Phe	Thr	Asn	Val	Asp	Asn	Tyr	Asp	Pro	Asp	Ile	Arg
				245					250					255	

Val	Lys	Asp	Pro	Asp	Val	Arg	Arg	Val	Ala	Thr	Thr	Gln	Pro	Arg	Gln
			260					265					270		

Trp	Tyr	His	Ala	Tyr	Gln	His	Ile	Tyr	Leu	Ala	Val	Leu	Tyr	Gly	Thr	275	280	285
Leu	Ala	Leu	Lys	Ser	Ile	Phe	Leu	Asp	Asp	Phe	Leu	Ala	Tyr	Phe	Thr	290	295	300
Gly	Ser	Ile	Gly	Pro	Val	Lys	Val	Ala	Lys	Met	Thr	Pro	Leu	Glu	Phe	305	310	315
Asn	Ile	Phe	Phe	Gln	Gly	Lys	Leu	Leu	Tyr	Ala	Phe	Tyr	Met	Phe	Val	325	330	335
Leu	Pro	Ser	Val	Tyr	Gly	Val	His	Ser	Gly	Gly	Thr	Phe	Leu	Ala	Leu	340	345	350
Tyr	Val	Ala	Ser	Gln	Leu	Ile	Thr	Gly	Trp	Met	Leu	Ala	Phe	Leu	Phe	355	360	365
Gln	Val	Ala	His	Val	Val	Asp	Asp	Val	Ala	Phe	Pro	Thr	Pro	Glu	Gly	370	375	380
Gly	Lys	Val	Lys	Gly	Gly	Trp	Ala	Ala	Met	Gln	Val	Ala	Thr	Thr	Thr	385	390	395
Asp	Phe	Ser	Pro	Arg	Ser	Trp	Phe	Trp	Gly	His	Val	Ser	Gly	Gly	Leu	405	410	415
Asn	Asn	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Gly	Val	Cys	His	Val	His	420	425	430
Tyr	Pro	Ala	Ile	Gln	Pro	Ile	Val	Glu	Lys	Thr	Cys	Lys	Glu	Phe	Asp	435	440	445
Val	Pro	Tyr	Val	Ala	Tyr	Pro	Thr	Phe	Trp	Thr	Ala	Leu	Arg	Ala	His	450	455	460
Phe	Ala	His	Leu	Lys	Lys	Val	Gly	Leu	Thr	Glu	Phe	Arg	Leu	Asp	Gly	465	470	475
																480		